STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/900, 963 B_
Source: _JFW16_
Date Processed by STIC: _12/15/2005_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/900, 963B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2____Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3_____Misaligned Amino The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
Numbering   use **space characters**, instead.

4_____Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
ensure your subsequent submission is saved in ASCII text.**

5_____Variable Length Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.**

7_____Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8_____Skipped Sequences Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
(NEW RULES)   <210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10_____Invalid <213> Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
is Artificial Sequence

11_____Use of <220> ~~Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.~~
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n/Xaa "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFW16

RAW SEQUENCE LISTING   DATE: 12/15/2005
PATENT APPLICATION: US/09/900,963B   TIME: 08:47:31

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   1 <110> APPLICANT: GUERIN-MARCHAND, CLAUDINE
   2   DRUILHE, PIERRE
   3 <120> TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE HEPATIC STAGES OF P.
FALCIPARUM
   4   BEARING EPITOPES CAPABLE OF STIMULATING THE T LYMPHOCYTES
   5 <130> FILE REFERENCE: 010830-118
C--> 6 <140> CURRENT APPLICATION NUMBER: US/09/900,963B
   7 <141> CURRENT FILING DATE: 2001-07-10
   8 <150> PRIOR APPLICATION NUMBER: 08/098,327
   9 <151> PRIOR FILING DATE: 1993-11-24
  10 <150> PRIOR APPLICATION NUMBER: PCT/FR92/00104
  11 <151> PRIOR FILING DATE: 1992-02-05
  12 <150> PRIOR APPLICATION NUMBER: FR 91 01286
  13 <151> PRIOR FILING DATE: 1991-02-05
  14 <160> NUMBER OF SEQ ID NOS: 47
  15 <170> SOFTWARE: PatentIn Ver. 3.3

_pp 1-2, 5, 7_

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

 768 <210> SEQ ID NO: 37
 769 <211> LENGTH: 954
 770 <212> TYPE: DNA
 771 <213> ORGANISM: Plasmodium falciparum
 772 <221> NAME/KEY: CDS
 773 <222> LOCATION: (1)..(954)
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 777   1   5   10   15
 778   ttg ata ttt cat ata aat gga aag ata ata aag aat tct gaa aaa gat   96
 779   Leu Ile Phe His Ile Asn Gly Lys Ile Ile Lys Asn Ser Glu Lys Asp
 780   20   25   30
 781   gaa atc ata aaa tct aac ttg aga agt ggt tct tca aat tct agg aat   144
 782   Glu Ile Ile Lys Ser Asn Leu Arg Ser Gly Ser Ser Asn Ser Arg Asn
 783   35   40   45
 784   cga ata aat gag gaa aat cac gag aag aaa cac gtt tta tct cat aat   192
 785   Arg Ile Asn Glu Glu Asn His Glu Lys Lys His Val Leu Ser His Asn
 786   50   55   60
 787   tca tat gag aaa act aaa aat aat gaa aat aat aaa ttt ttc gat aag   240
 788   Ser Tyr Glu Lys Thr Lys Asn Asn Glu Asn Asn Lys Phe Phe Asp Lys
 789   65   70   75   80
 790   gat aaa gag tta acg atg tct aat gta aaa aat gtg tca caa aca aat   288
 791   Asp Lys Glu Leu Thr Met Ser Asn Val Lys Asn Val Ser Gln Thr Asn

Insert
> < 220> whenever < 221>, < 222 >
_or_
_< 223> is_
Shown
_< 220>_
never
has a
response
_it is a_
header
only.

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793      ttc aaa agt ctt tta aga aat ctt ggt gtt tca gag aat ata ttc ctt    336
794      Phe Lys Ser Leu Leu Arg Asn Leu Gly Val Ser Glu Asn Ile Phe Leu
795                  100               105               110
796      aaa gaa aat aaa tta aat aag gaa ggg aaa tta att gaa cac ata ata    384
797      Lys Glu Asn Lys Leu Asn Lys Glu Gly Lys Leu Ile Glu His Ile Ile
798                  115               120               125
799      aat gat gat gac gat aaa aaa aaa tat att aaa ggg caa gac gaa aac    432
800      Asn Asp Asp Asp Asp Lys Lys Lys Tyr Ile Lys Gly Gln Asp Glu Asn
801          130               135               140
802      aga caa gaa gat ctt gaa gaa aaa gca gct aaa gaa aag tta cag ggg    480
803      Arg Gln Glu Asp Leu Glu Glu Lys Ala Ala Lys Glu Lys Leu Gln Gly
804      145               150               155               160
805      caa caa agc gat tca gaa caa gag aga cgt gct aaa gaa aag ttg caa    528
806      Gln Gln Ser Asp Ser Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln
807                  165               170               175
808      gaa caa caa agc gat tta gaa caa gag aga ctt gct aaa gaa aag ttg    576
809      Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys Glu Lys Leu
810                  180               185               190
811      caa gaa caa caa agc gat tta gaa caa gag aga cgt gct aaa gaa aag    624
812      Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys
813                  195               200               205
814      ttg caa gaa caa caa agc gat tta gaa caa gag aga ctt gct aaa gaa    672
815      Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys Glu
816          210               215               220
817      aag ttg caa gaa caa caa agc gat tta gaa caa gag aga cgt gct aaa    720
818      Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys
819      225               230               235               240
820      gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag aga cgt gct    768
821      Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala
822                  245               250               255
823      aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag aga ctt    816
824      Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu
825                  260               265               270
826      gct aaa gaa aag tta caa gag cag caa agc gat tta gaa caa gat aga    864
827      Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg
828                  275               280               285
829      ctt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag    912
830      Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu
831          290               295               300
832      aga cgt gct aaa gaa agg ttg caa gaa caa caa agc gat tta            954
833      Arg Arg Ala Lys Glu Arg Leu Gln Glu Gln Gln Ser Asp Leu
834          305               310               315
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927 <210> SEQ ID NO: 42
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929 <212> TYPE: DNA
930 <213> ORGANISM: Plasmodium falciparum
931 <221> NAME/KEY: CDS
932 <222> LOCATION: (1)..(1494)

Insert
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     936       1               5                  10                  15
     937      ttg caa gaa caa caa agc gat tta gaa caa gat aga ctt gct aaa gaa   96
     938      Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu
     939                     20                  25                  30
     940      aag tta caa gag cag caa agc gat tta gaa caa gag aga ctt gct aaa   144
     941      Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys
     942                  35                  40                  45
     943      gaa aag ttg caa gaa caa caa agc gat cta gaa caa gag aga cgt gct   192
     944      Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala
     945           50                  55                  60
     946      aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag aga cgt   240
     947      Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg
     948        65                  70                  75                  80
     949      gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gat aga   288
     950      Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg
     951                     85                  90                  95
     952      ctt gct aaa gaa aag tta caa gag cag caa agc gat tta gaa caa gag   336
     953      Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu
     954                  100                 105                 110
     955      aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa   384
     956      Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln
     957                  115                 120                 125
     958      gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa   432
     959      Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu
     960                  130                 135                 140
     961      caa gag aga ctt gct aaa gaa aag ttg caa gaa caa caa agc gat tta   480
     962      Gln Glu Arg Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu
     963      145                 150                 155                 160
     964      gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat   528
     965      Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp
     966                  165                 170                 175
     967      tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc   576
     968      Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser
     969                  180                 185                 190
     970      gat tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gag cag caa   624
     971      Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln
     972                  195                 200                 205
     973      aga gat tta gaa caa agg aag gct gat acg aaa aaa aat tta gaa aga   672
     974      Arg Asp Leu Glu Gln Arg Lys Ala Asp Thr Lys Lys Asn Leu Glu Arg
     975      210                 215                 220
     976      aaa aag gaa cat gga gat ata tta gca gag gat tta tat ggt cgt tta   720
     977      Lys Lys Glu His Gly Asp Ile Leu Ala Glu Asp Leu Tyr Gly Arg Leu
     978      225                 230                 235                 240
     979      gaa ata cca gct ata gaa ctt cca tca gaa aat gaa cgt gga tat tat   768
     980      Glu Ile Pro Ala Ile Glu Leu Pro Ser Glu Asn Glu Arg Gly Tyr Tyr
     981                  245                 250                 255
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982    ata cca cat caa tct tct tta cct cag gac aac aga ggg aat agt aga   816
983    Ile Pro His Gln Ser Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg
984            260             265             270
985    gat tcc aag gaa ata tct ata ata gaa aaa aca aat aga gaa tct att   864
986    Asp Ser Lys Glu Ile Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile
987            275             280             285
988    aca aca aat gtt gaa gga cga agg gat ata cat aaa gga cat ctt gaa   912
989    Thr Thr Asn Val Glu Gly Arg Arg Asp Ile His Lys Gly His Leu Glu
990            290             295             300
991    gaa aag aaa gat ggt tca ata aaa cca gaa caa aaa gaa gat aaa tct   960
992    Glu Lys Lys Asp Gly Ser Ile Lys Pro Glu Gln Lys Glu Asp Lys Ser
993    305             310             315             320
994    gct gac ata caa aat cat aca tta gag aca gta aat att tct gat gtt   1008
995    Ala Asp Ile Gln Asn His Thr Leu Glu Thr Val Asn Ile Ser Asp Val
996            325             330             335
997    aat gat ttt caa ata agt aag tat gag gat gaa ata agt gct gaa tat   1056
998    Asn Asp Phe Gln Ile Ser Lys Tyr Glu Asp Glu Ile Ser Ala Glu Tyr
999            340             345             350
1000   gac gat tca tta ata gat gaa gaa gaa gat gat gaa gac tta gac gaa   1104
1001   Asp Asp Ser Leu Ile Asp Glu Glu Glu Asp Asp Glu Asp Leu Asp Glu
1002            355             360             365
1003   ttt aag cct att gtg caa tat gac aat ttc caa gat gaa gaa aac ata   1152
1004   Phe Lys Pro Ile Val Gln Tyr Asp Asn Phe Gln Asp Glu Glu Asn Ile
1005            370             375             380
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1007   Gly Ile Tyr Lys Glu Leu Glu Asp Leu Ile Glu Lys Asn Glu Asn Leu
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1009   gat gat tta gat gaa gga ata gaa aaa tca tca gaa gaa tta tct gaa   1248
1010   Asp Asp Leu Asp Glu Gly Ile Glu Lys Ser Ser Glu Glu Leu Ser Glu
1011            405             410             415
1012   gaa aaa ata aaa aaa gga aag aaa tat gaa aaa aca aag gat aat aat   1296
1013   Glu Lys Ile Lys Lys Gly Lys Lys Tyr Glu Lys Thr Lys Asp Asn Asn
1014            420             425             430
1015   ttt aaa cca aat gat aaa agt ttg tat gat gag cat att aaa aaa tat   1344
1016   Phe Lys Pro Asn Asp Lys Ser Leu Tyr Asp Glu His Ile Lys Lys Tyr
1017            435             440             445
1018   aaa aat gat aag cag gtt aat aag gaa aag gaa aaa ttc ata aaa tca   1392
1019   Lys Asn Asp Lys Gln Val Asn Lys Glu Lys Glu Lys Phe Ile Lys Ser
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1021   ttg ttt cat ata ttt gac gga gac aat gaa att tta cag atc gtg gat   1440
1022   Leu Phe His Ile Phe Asp Gly Asp Asn Glu Ile Leu Gln Ile Val Asp
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1024   gag tta tct gaa gat ata act aaa tat ttt atg aaa cta taa aag gtt   1488
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1113 <212> TYPE: DNA
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RAW SEQUENCE LISTING   DATE: 12/15/2005
PATENT APPLICATION: US/09/900,963B   TIME: 08:47:31

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1116 <222> LOCATION: (1)..(1494)
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1120      1               5                   10                  15
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1122      Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu
1123                      20                  25                  30
1124      aag tta caa gag cag caa agc gat tta gaa caa gag aga ctt gct aaa   144
1125      Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys
1126                  35                  40                  45
1127      gaa aag ttg caa gaa caa caa agc gat cta gaa caa gag aga cgt gct   192
1128      Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala
1129                  50                  55                  60
1130      aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag aga cgt   240
1131      Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg
1132      65                  70                  75                  80
1133      gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gat aga   288
1134      Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg
1135                      85                  90                  95
1136      ctt gct aaa gaa aag tta caa gag cag caa agc gat tta gaa caa gag   336
1137      Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu
1138                  100                 105                 110
1139      aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa   384
1140      Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln
1141                  115                 120                 125
1142      gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa   432
1143      Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu
1144                  130                 135                 140
1145      caa gag aga ctt gct aaa gaa aag ttg caa gaa caa caa agc gat tta   480
1146      Gln Glu Arg Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu
1147      145                 150                 155                 160
1148      gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat   528
1149      Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp
1150                  165                 170                 175
1151      tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc   576
1152      Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser
1153                  180                 185                 190
1154      gat tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gag cag caa   624
1155      Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln
1156                  195                 200                 205
1157      aga gat tta gaa caa agg aag gct gat acg aaa aaa aat tta gaa aga   672
1158      Arg Asp Leu Glu Gln Arg Lys Ala Asp Thr Lys Lys Asn Leu Glu Arg
1159                  210                 215                 220
1160      aaa aag gaa cat gga gat ata tta gca gag gat tta tat ggt cgt tta   720
1161      Lys Lys Glu His Gly Asp Ile Leu Ala Glu Asp Leu Tyr Gly Arg Leu
1162      225                 230                 235                 240
```

```
1163    gaa ata cca gct ata gaa ctt cca tca gaa aat gaa cgt gga tat tat    768
1164    Glu Ile Pro Ala Ile Glu Leu Pro Ser Glu Asn Glu Arg Gly Tyr Tyr
1165                    245                 250                 255
1166    ata cca cat caa tct tct tta cct cag gac aac aga ggg aat agt aga    816
1167    Ile Pro His Gln Ser Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg
1168                    260                 265                 270
1169    gat tcc aag gaa ata tct ata ata gaa aaa aca aat aga gaa tct att    864
1170    Asp Ser Lys Glu Ile Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile
1171            275                 280                 285
1172    aca aca aat gtt gaa gga cga agg gat ata cat aaa gga cat ctt gaa    912
1173    Thr Thr Asn Val Glu Gly Arg Arg Asp Ile His Lys Gly His Leu Glu
1174            290                 295                 300
1175    gaa aag aaa gat ggt tca ata aaa cca gaa caa aaa gaa gat aaa tct    960
1176    Glu Lys Lys Asp Gly Ser Ile Lys Pro Glu Gln Lys Glu Asp Lys Ser
1177    305                 310                 315                 320
1178    gct gac ata caa aat cat aca tta gag aca gta aat att tct gat gtt    1008
1179    Ala Asp Ile Gln Asn His Thr Leu Glu Thr Val Asn Ile Ser Asp Val
1180                    325                 330                 335
1181    aat gat ttt caa ata agt aag tat gag gat gaa ata agt gct gaa tat    1056
1182    Asn Asp Phe Gln Ile Ser Lys Tyr Glu Asp Glu Ile Ser Ala Glu Tyr
1183                    340                 345                 350
1184    gac gat tca tta ata gat gaa gaa gaa gat gat gaa gac tta gac gaa    1104
1185    Asp Asp Ser Leu Ile Asp Glu Glu Glu Asp Asp Glu Asp Leu Asp Glu
1186            355                 360                 365
1187    ttt aag cct att gtg caa tat gac aat ttc caa gat gaa gaa aac ata    1152
1188    Phe Lys Pro Ile Val Gln Tyr Asp Asn Phe Gln Asp Glu Glu Asn Ile
1189            370                 375                 380
1190    gga att tat aaa gaa cta gaa gat ttg ata gag aaa aat gaa aat tta    1200
1191    Gly Ile Tyr Lys Glu Leu Glu Asp Leu Ile Glu Lys Asn Glu Asn Leu
1192    385                 390                 395                 400
1193    gat gat tta gat gaa gga ata gaa aaa tca tca gaa gaa tta tct gaa    1248
1194    Asp Asp Leu Asp Glu Gly Ile Glu Lys Ser Ser Glu Glu Leu Ser Glu
1195                    405                 410                 415
1196    gaa aaa ata aaa aaa gga aag aaa tat gaa aaa aca aag gat aat aat    1296
1197    Glu Lys Ile Lys Lys Gly Lys Lys Tyr Glu Lys Thr Lys Asp Asn Asn
1198                    420                 425                 430
1199    ttt aaa cca aat gat aaa agt ttg tat gat gag cat att aaa aaa tat    1344
1200    Phe Lys Pro Asn Asp Lys Ser Leu Tyr Asp Glu His Ile Lys Lys Tyr
1201            435                 440                 445
1202    aaa aat gat aag cag gtt aat aag gaa aag gaa aaa ttc ata aaa tca    1392
1203    Lys Asn Asp Lys Gln Val Asn Lys Glu Lys Glu Lys Phe Ile Lys Ser
1204            450                 455                 460
1205    ttg ttt cat ata ttt gac gga gac aat gaa att tta cag atc gtg gat    1440
1206    Leu Phe His Ile Phe Asp Gly Asp Asn Glu Ile Leu Gln Ile Val Asp
1207    465                 470                 475                 480
1208    gag tta tct gaa gat ata act aaa tat ttt atg aaa cta taa aag gtt    1488
1209    Glu Leu Ser Glu Asp Ile Thr Lys Tyr Phe Met Lys Leu
1210                    485                 490
1211    ata tat                                                            1494
```

```
<210> 1
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Formula Sequence

<220>
<221> VARIANT
<222> 8
<223> Xaa = Glu or Gly

<400> 1
Leu Ala Lys Glu Lys Leu Gln Xaa Gln Gln Ser Asp Leu Glu Gln Glu
 1               5                  10                 15
Arg
```

Insufficient Explanation. Give Source(s) of genetic material (See item 11 on Error Summary Sheet).

The above is a Sample of Global Error

P41

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/15/2005
PATENT APPLICATION: **US/09/900,963B**   TIME: 08:47:32

Input Set : **N:\Crf4\Refhold\09_folder\I900963B.raw**
Output Set: **N:\CRF4\12152005\I900963B.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 3

VERIFICATION SUMMARY   DATE: 12/15/2005
PATENT APPLICATION: **US/09/900,963B**   TIME: 08:47:32

Input Set : **N:\Crf4\Refhold\09_folder\I900963B.raw**
Output Set: **N:\CRF4\12152005\I900963B.raw**

```
L:6 M:270 C: Current Application Number differs, Wrong Format
L:28 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:38 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:16
L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:16
L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:16
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:460 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:16
L:774 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:37
L:933 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:42
L:1117 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:46
```